

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2000, 14:05:12 ; Search time 14.9 Seconds
(without alignments)
668.675 Million cell updates/sec

Title: US-09-373-230-2

Perfect score: 808

Sequence: 1 NFGRLHCTAVIRNINDQVL.....KKDENGKSVAFITLNLHQS 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-65:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	806	99.8	192	2	S60226
2	82.5	10.2	803	1	A64070
3	82	10.1	267	1	JN0724
4	81	10.0	483	2	T21327
5	80.5	10.0	267	2	S38373
6	80	9.9	506	2	D71461
7	79.5	9.8	526	2	A41698
8	78.5	9.7	1039	2	E72734
9	78	9.7	1196	2	J01467
10	78	9.7	1196	2	S46430
11	78	9.7	1247	2	E71616
12	77.5	9.6	366	2	T30457
13	77	9.5	266	1	ICB01B
14	77	9.5	563	2	T09378
15	76.5	9.2	157	2	A64401
16	76.5	9.5	621	2	B64546
17	76.5	9.5	705	2	S38168
18	76.5	9.5	905	2	T39572
19	76.5	9.5	1294	2	T48349
20	76	9.4	525	2	T43437
21	75.5	9.3	270	1	ICMS1
22	75.5	9.3	439	2	C64401
23	75.5	9.3	626	2	T35669
24	75.5	9.3	695	2	F64135
25	75.5	9.3	866	2	T06454
26	75	9.3	266	1	S23010
27	75	9.3	621	2	A71961
28	75	9.3	624	2	S67382
29	75	9.3	1146	2	E70204

30	74.5	9.2	270	1	S10532	interleukin-1 alph
31	74.5	9.2	661	2	S75005	sensory transducti
32	74	9.2	254	2	E70230	conserved hypothet
33	74	9.2	269	1	ICB01B	interleukin-1 beta
34	74	9.2	318	2	C81447	chemotaxis protein
35	74	9.2	322	2	T48460	MADS-box protein-1
36	74	9.2	488	2	T45041	hypothetical prote
37	74	9.2	1139	2	A49370	E1A-associated cyc
38	73.5	9.1	589	2	C72414	anthranilate synth
39	73.5	9.1	647	2	S61973	hypothetical prote
40	73.5	9.1	680	2	T39859	hypothetical prote
41	73.5	9.1	1146	2	T09112	probable sensor ki
42	73.5	9.1	2077	2	T43991	large tegument pro
43	73.5	9.1	2077	2	T44178	large tegument pro
44	73	9.0	611	2	S38162	translation elonga
45	73	9.0	872	1	P2XRCW	RNA-binding protei

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torii
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:9606109
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OK>
A:Cross-references: EMBL:D49949; NID:q1064822; PIDN:BAA08705.1; PID:q1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 99.8%; Score 806; DB 2; Length 192;
Best local similarity 99.4%; Pred. No. 1.9e-65;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFGRLHCTAVIRNINDQVLFEVDKRPVEDMTDIDQASBPOTRLIYMYDSEVRLA 60
DB 36 NFGRLHCTAVIRNINDQVLEFVDKRPVEDMTDIDQASBPOTRLIYMYDSEVRLA 95
QY 61 VTLSVSKSKSTLCKNKTIISFEEMPPENIDIDSDIFQKRVGRCHKMEFESSLYEG 120
DB 96 VTLSVSKSKSTLCKNKTIISFEEMPPENIDIDSDIFQKRVGRCHKMEFESSLYEG 155
QY 121 HFLACQKEDDAFKLLKKRDKDNGSKSVMTLNLHQS 157
DB 156 HFLACQKEDDAFKLLKKRDKDNGSKSVMTLNLHQS 192

RESULT 2
A64070
endopeptidase Ia (EC 3.4.21.53) - Haemophilus influenzae (strain Rd Kw20)
N:Alternate names: App-dependent proteinase I; App-dependent serine proteinase Ia
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Haemophilus influenzae
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 18-Jun-1999
C:Accession: A64070
R:Feleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirschner, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: A64070

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-803 <TRIG>
A:Cross-references: GB:U022729; GB:I42023; NID:g1573439; PIDN:MAC22121.1; PID:g1573440; T
C:Comment: This allosteric enzyme catalyzes the hydrolysis of large proteins in the pres
C:Genetics:
A:Gene: lon; lon-A
C:Superfamily: ATP-dependent serine proteinase Ia
C:Keywords: allosteric regulation; ATP; DNA binding; heat shock; hydrolase; P-loop; ser; ser
F:356-363/Region: nucleotide-binding motif A (P-loop)
F:419-424/Region: nucleotide-binding motif B
F:679/Active site: Ser #status predicted

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Query Match      10.2%: Score 82.5; DB 1; Length 803;
Best Local Similarity 18.9%: Pred. No. 10;
Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

QY      3  GRHCTAVIIRIND--OVLEVDKR---OPVEDMTDIDQAS-----40
      |||  :||  |||  :||  :||  :||  :||  :||  :||  :||
Db      30  GRASINALEAMDDKKIILVSGREADLEETPEEDVGITIANIIQLKLPDPTKAVL  89
      |||  :||  |||  :||  :||  :||  :||  :||  :||  :||

QY      41  -EPQTRLIIYWKQSE-----VRELATLVSXKSKSTLSCKNNIIIFE  83
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||
Db      90  VEGGNRAIINSLDEQKCFSAQITPIETTYGDEKELVAKSAVISEFNITLTKNKVPTD  149
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||

QY      84  EMDPENIDDI-----QSDLIFFQK  103
      :||  :||  :||  :||  :||  :||  :||  :||  :||  :||
Db      150  ILNLQRIDVDRLADTWAHLPVSIIRKQALELANVOERLEYLLGMSESEADITLYQEK  209
      :||  :||  :||  :||  :||  :||  :||  :||  :||  :||

QY      104  RVPGHNKKEFFESLYEGHFPLAQCKEDDAFKILKKKIDGNKSVAFITLTLNHQ  156
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||
Db      210  RIRIRVAKQMKRS-QRNTYL-----NEQIKRIRKMDGEGENEDTIDVEQJLHQ  256
      |||  :||  :||  :||  :||  :||  :||  :||  :||  :||

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RESULT 3
JN0724
Interleukin-1 beta precursor - pig
N:Alternate names: hematopoietin-1, IL-1 beta
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C:Accession: JN0724
R:Huetheer, M.J.; Lin, G.; Smith, D.M.; Murttaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta
A:Accession number: JN0724; MUID:93314975
A:Reference: JN0724
A:Molecule type: mRNA
A:Residues: 1-267 <HUE>
A:Cross-references: GB:886725; NID:g164607; PIDN:AAA02584.1; PID:g164608
A:Experimental source: alveolar macrophage
C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes involved in the development of the immune system. It is a member of the interleukin-1 family. The deduced form of interleukin-1beta, unlike interleukin-1alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1alpha.
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage
E:115-267/Product: interleukin-1 beta #status predicted <IL1>
F:77/Binding site: myristate (uys) (covalent) #status predicted

```

Query Match	10.1%;	Score 82;	DB 1;	Length 267;
Best Local Similarity	26.1%;	Pred. No. 3.2;		
Matches	23;	Conservative	22;	Mismatches 31;
				Indels 12;
				Gaps 5;

```
QY      49 YMKKDSFVAGLAVTLVKDKXSTLSCKNK----IISFEEMP---PENIDIQSLIF 101
          :: - : ||| :-| ||| | : |||| | : |:: :-|
Db     160 FVGDDSNKKIPVLGIK-GKNLYLSCVMKDNTPTQLTEDIDPKRYPKR--DMEKREVFY 216
```

OY 10Z QKRVPGHNKMEFESSLYEGHFLACQKED 129
: : ||:|||||:
PH 217 KTEI--KNRVEFESALYPNWTISTSQA E 242

RESULT 4
T21327
hypothetical protein F25C8.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21327
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19407
A:Accession: T21327
A:status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-483 <MIL>
A:Cross-references: EMBL:281512; PIDN:CAB04171.1; GSPDB:GM00023; CESP:F25C8.2
A:Experimental source: clone F25C8
C:Genetics:
A:Gene: CESP:F25C8.2
A:Map position: 5
A:Introns: 13/2; 136/2; 209/3; 358/3; 444/2

```

Query Match 10.0% Score 81: DB 2: Length 483,
Best Local Similarity 26.4%: Pred No. 7.8;
Matches 55; Conservative 24; Mismatches 63; Indels 66; Gaps 12.

QY      3  GRHCTTAVIRINDOV-----LEVDKRPVEDMTDIDOSAS-----EPQRLII 48
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      81  GYLHGAEEVYVNGDVNDENVYMLVEKYDLF-DKTPRPRIIDMLDQNSIFLVNGHLPVKLI 139

QY      49  YMKDSEVRGLAVLTYSVKDSKXSTSCCKKIIS-FEEM--DPRENIDDLQSLIFFOKRY 105
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     140  DKFND-YIYLVNVALYEKIKINQLSVEENINNOFTFLRPDPENDHETYESLVNVR-- 196

QY      106  PGHNMKEEFSSLYEGHFL-----ACQEKEDA-----FKLILK----- 137
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     197  ---NFQOTEMSSPVELSLNSLNIWDGDEEEDSAVLNKGFEYLKDPFRSKIPAGNIRL 253

QY      138  -----KKDENGDKSYMFTLTN-----LH 155
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     254  NCEVINVKEEN-----INVTLNNGEYVL 277

```

RESULT 5
S38373
Interleukin-1 beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C:Accession: S38373
R:Vandenbroeck, K.; Filten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
Eurt, J. Blochem. 217, 45-52, 1993
A:Title: Gene sequence, cDNA construction, expression in *Escherichia coli* and genetic
A:Reference number: S38373; MUID:94039070
A:Accession: S38373
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <VAN>
A:Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C:Genetics:
A:Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C:Superfamily: Interleukin-1

Query Match	10.0%	Score 80.5;	DB 2;	Length 267;
Best Local Similarly	28.6%	Pred. No. 4.3;		
Matches 24;	Conservative 22;	Mismatches 25;	Indels 13;	Gaps 6;

QY 53 DSEVRLGLAVTLSVKDKSKSTLSCNK----IIFFEEMDP--PEINIDIOSDLIFEOKRV 105
|| : : ||| : | ||| | : ||| | : || :
Dd 165 DSDDK-IPVTLGIG-KNLYLSCVMKDPTLTLEDVDPKSYPRK-DMEKRFFVFYKEI 220

```

QY      106 PGHNKMEFESSLYEGHFLACQED 129
      |::|||::||      :::  : :

```

Db 221 --KNRVEFSALYPMWYISTSQAE 242

RESULT 6
D71461
hypothetical protein CT861 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: D71461
R:Stephens, R.S.; Kalman, S.; Lamell, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809
A:Accession: D71461
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1506 <ARN>
A:Cross-references: GB:AE001359; GB:AE001273; NID:g3329331; PIDN:AAC68459.1; PID:g332933
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics: CT861
A:Gene: CT861

Query Match 9.9%; Score 80; DB 2; Length 506;
Best Local Similarity 25.0%; Pred. No. 10;
Matches 36; Conservative 25; Mismatches 55; Indels 34; Gaps 7;
QY 1 NGRHCTTAATVIRINDOYLVDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVGLA 60
DB 63 SFSRLQPTTP-----KERLFFGS-SPSSQLSTVATTTSSPMN-----LFSNSQTRNST 111
QY 61 VTLVSKDKKXSTLSCKN-KITSEEMDPENIDIDQSLDIFFOKRVPGHKKMFESSLY 118
DB 112 KRLSEKLFSSSELSARDSTKPSSEPTKPSNL-----LHPEHHR-ELFSSLK 159
QY 119 EGHFLACQKEDDAF-----KLKKRDE 141
DB 160 KDNLSPIMERIDFSFSETSELESLERLVTKKEE 191

RESULT 7
A1698
cell division control protein CDC55 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G1345; protein YGL190c
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 29-Oct-1999
C:Accession: A41698; S31274; S61128; S62055; S64207; S18513
R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; Depaulis-Roach, A.A.; Pringle, M.L. Cell. Biol. 11, 5767-5780, 1991
A:Title: CDC55, a Saccharomyces cerevisiae gene involved in cellular morphogenesis: identification
A:Reference number: A41698; MUID:92017858
A:Accession: A41698
A:Molecule type: DNA
A:Residues: 1526 <HEA1>
A:Cross-references: GB:M72716
A:Note: the authors translated the codon TAT for residue 116 as Val and CCT for residue 119
R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; Depaulis-Roach, A.A.; Pringle, M.L. submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cerevisiae new genes.
A:Reference number: S31274
A:Accession: S31274
A:Molecule type: DNA
A:Residues: 1499; N', 501-526 <HEA2>
A:Cross-references: EMBL:M72716; PIDN:AAA34482.1; PID:g171195
R:Bernt, I.; Cogliavina, M.; Zaccaria, P.; Klima, R.; Brusch, C.V.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cerevisiae new genes.
A:Reference number: S61128
A:Accession: S61128
A:Molecule type: DNA
A:Residues: 1281 <BER>
A:Cross-references: EMBL:X91489; NID:g1143557; PIDN:CAA62785.1; PID:g199121; PID:g114355
R:Cogliavina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bernt, I.; Brusch, C.V.

submitted to the EMBL Data Library, September 1995
A:Description: A 6.7 kb fragment from chromosome VII of Saccharomyces cerevisiae cont
A:Reference number: S62055
A:Accession: S62055
A:Molecule type: DNA
A:Residues: 283-526 <COG>
A:Cross-references: EMBL:X91837; NID:g117627; PIDN:CAA62954.1; PID:g203624; PID:g117
R:Brusch, C.V.; Cogliavina, M.; Bernt, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64183
A:Accession: S64207
A:Molecule type: DNA
A:Residues: 1526 <BRU>
A:Cross-references: EMBL:M72712; NID:g1322810; PIDN:CAA69602.1; PID:g243794; PID:g132
A:Experimental source: strain S288C
C:Genetics: S288C
A:Gene: S288C
A:Cross-references: SGD:S0003158; MIPS:YGL190c
A:Map position: 7L

Query Match 9.8%; Score 79.5; DB 2; Length 526;
Best Local Similarity 25.0%; Pred. No. 12;
Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;
QY 14 NINDOYL-FVDRKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVGLAATLSVKDKXST 72
DB 213 DIPQSNIVDILKPTNMELETVITSAEPHPCNLFMISSK-----GTIKCDMKRNS 267
QY 73 LSCKNKITSEEMDPENIDIDQSLDIFFOKRVPGHKKMFESSLYEGHFLACQKEDDAF 132
DB 268 L-CDNKRTTFFEEYDIPNHN-----FTEITTSIDIRKSPN---GRYASRD----- 311
QY 133 KLKKRDEGDKSVMTLTNLHQ 156
DB 312 YLVKIMDVNMNKKPLKTI-NIHE 334

RESULT 8
E72734
hypothetical protein APE0413 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 17-Mar-2000
C:Accession: E72734
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Tawa, H.; Takaiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: E72734
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 11039 <KAW>
A:Cross-references: DBJ:AP000059; NID:g5103911; PIDN:BAA79369.1; PID:d1043155; PID:g
A:Experimental source: strain K1
C:Genetics: APE0413
A:Gene: APE0413
C:Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology

Query Match 9.7%; Score 78.5; DB 2; Length 1039;
Best Local Similarity 26.4%; Pred. No. 37;
Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;
QY 31 DMDIDQASSEPOTRLIITYMKDSEVGLAATLSVKDKXSTL 73
DB 374 DIGIDEDEDEFEERLAIYFPKLLDDMFRELKKAQYAEIDLGVKAV-----DSKVERL 428
QY 74 SCKNKITSEEMDPENIDIDQSLDIFFOKRVPGHKKMFESSLYEGHFLACQKEDDAF 133
DB 429 ----KTLGLVLTTPPEEDPEFRDLA-SQNAIVTFEFNDATYLYE-----K 471

Db 91 NATVYVNPILPIGEV---GVGDFRVSVLLTNDLFCNTMIIGHDIVSPVEFRTNVN 146
 Oy 119 EGHFLACQKEDDAFKLLKKKENGKSVFTL 151
 Db 147 YKKLPTEAEDEPLFNKRLRDDNDNDFLCKFL 179

RESULT 13

ICBO1B
 Interleukin-1 beta precursor - bovine
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C:Accession: J00010; S01380
 R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988
 A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin 1-beta
 A:Reference number: A94695; M01D:88318652
 A:Accession: J00010
 A:Molecule type: mRNA
 A:Residues: 1-266 <MAL>
 R:Cross-References: GB:M37211; NID:9163200; PIDN:AAA30584.1; PID:9163201
 R:Cloning, S.R.; Flagg, G.W.; Lammann, M.; Gray, P.W.
 A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
 A:Reference number: S01380; M01D:89016591
 A:Accession: S01380
 A:Molecule type: mRNA
 A:Residues: 1-251; A: 253-266 <LEO>
 A:Cross-References: EMBL:X12498; NID:94448; PIDN:CAA31018.1; PID:94449
 C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and involved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
 C:Keywords: Cytokine; Immunoregulation; Inflammation; Lymphokine; macrophage; mitogen
 F:114-266/Product: Interleukin-1 beta #status Predicted <MAT>

Query Match 9.5%; Score 77; DB 1; Length 266;
 Best Local Similarity 26.0%; Pred. No. 8.9;
 Matches 27; Conservative 24; Mismatches 33; Indels 20; Gaps 7;
 Oy 40 SEPTRLIYMYKXSEVRG-----IAVTLVSKSKSTSCNK-----IIFEDMDP-- 87
 Db 146 SEQMREYVFCM--SFQGBERMKIPVALGKD-KMLVLCYKKGDTPTLDLEVDKXV 202
 Oy 88 -PENDDIOSDLFFQKRVGHNKMEFESSLYEGHFLACQKED 130
 Db 203 YPKR--NMEKRFVFKTEI--KNYEFESVLYPMWYISTQIEE 242

RESULT 14

T09378
 Hypothetical protein F23K16.250 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C:Accession: T09378
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16652
 A:Accession: T09378
 A:Molecule type: DNA
 A:Residues: 1-563 <BEV>
 A:Cross-References: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250
 A:Experimental source: cultivar Columbia; BAC clone F23K16
 C:Genetics:
 A:Gene: ATSP:F23K16.250
 A:Map position: 4
 A:Introns: 118/3; 502/3

Query Match 9.5%; Score 77; DB 2; Length 563;

Best Local Similarity 23.6%; Pred. No. 21;
 Matches 33; Conservative 29; Mismatches 40; Indels 38; Gaps 7;
 Oy 22 VDKROPVEDMDTIDOSAS--EPQTRLIYMYKXSEVRGLAVTLVSKDS---KXSTLS- 74
 Db 329 IDKAEVVFKKMNDMYIPSFITYECMIMWYCGSVSRARIPFEVGESEDRVLKASTLNA 388
 Oy 75 -----CKNKIIFSEMDPENIDIOSDLFFQKRVPGHNKMEF---ESSLYEGHFLAC 125
 Db 389 MLEVYCRNGLY-----LEADKL-----HNSARVHPDASTYKFLYKAY 428
 Oy 126 OKED--DAFKLLKKKDENG 143
 Db 429 TKADMKEGYQVILMKKMEKDG 448

RESULT 15

A64401
 Hypothetical protein M0809 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
 C:Accession: A64401
 R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 ; Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weisskopf, K.G.; Merrick, J.M.; Glodek,
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
 A:Reference number: A64300; M01D:96337999
 A:Accession: A64401
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-167 <BDL>
 A:Cross-References: GB:U67525; GB:L77117; NID:91591497; PIDN:AAB98817.1; PID:91499632
 C:Genetics:
 A:Map position: FOR733027-733530

Query Match 9.5%; Score 76.5; DB 2; Length 167;
 Best Local Similarity 26.8%; Pred. No. 5.7;
 Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;
 Oy 47 ILYMYKXSEVRGLAVTLVSKD-----XSTLCKNKIIFSEMDP-----PENID 92
 Db 38 ILYMYKXSEVRGLAVTLVSKD-----XSTLCKNKIIFSEMDP-----PENID 92
 Oy 93 DIOSDLFFQKRVGHNKMEFESSLYEGHFLACQKEDDAFKLLKKKDENGKSVFTL 152
 Db 98 RUSDDI-----LELNKRLDEG-----VKYILIFALDEH--KVVILEIK 136
 Oy 153 NLH 155
 Db 137 DMH 139

Search completed: November 20, 2000, 14:07:18
 Job time: 126 sec

